

StringBio 2018: Program

[Harris Corporation Engineering Center](#), Room 101,
University of Central Florida, Orlando, FL

Thursday, October 25, 2018

Opening Ceremony	
(9:00 - 9:30) Welcome	Shibu Yooseph
(9:30 - 10:30) Keynote	Martin Farach - Colton : The suffix Tree

(10:30 - 10:50)	Coffee Break
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Session I	
(10:50 - 12:20) Tutorial	Solon Pissis : Advanced Data Structures for Sequence Analysis
(12:20 - 12:40)	Patrick Flick : Parallel, Distributed-Memory String Indexes - Efficient Construction, and Querying

(12:40 - 14:00)	Lunch Break
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Session II	
(14:00 - 14:45) Tutorial	Oğuzhan külekci : Data Compression and its Application in Biological Data Management
(14:45 - 15:15) Tutorial	Alan Kuhnle : Genome Indexing and the Burrows-Wheeler Transform

(15:15 - 15:40)	Break
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Session III	
(15:40 - 16:10) Tutorial	Arnab Ganguly : Approximate Pattern Matching and Bidirectional Burrows-Wheeler Transform with Applications
(16:10 - 16:35)	Michael Kirsche : Suffix Array Piecewise Linear Index for Genomics
(16:35 - 17:00)	Sairam Behera : Suffix Tree Approach to Discover Conserved Non-Coding Sequences in Plants

Friday, October 26, 2018

Session I	
(9:00 - 10:00) Tutorial	Brian Brubach : Bloom Filters, Minhashes and Other Random Stuff
(10:00 - 11:00) Keynote	Srinivas Aluru : Long Read Mapping at Scale: Algorithms and Applications

(11:00 - 11:20)	Coffee Break
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Session II	
(11:20 - 11:40)	Bahar Alipanahi : Debruijn Graphs and its Applications in Genome Assembly and Variant Calling
(11:40 - 12:20) Tutorial	Diego Diez : Succinct Debruijn Graphs
(12:20 - 12:40)	Vicky Zheng : Mobile Computing for Connected Components in Streamed Metagenomics Minion Reads

(12:40 - 14:00)	Lunch Break
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Session III

(14:00 – 15:00) Keynote	Giri Narasimhan : Causality and Dynamics in Microbiomes
(15:00 – 15:20)	Break

Session IV

(15:20 – 15:40)	Dan DeBlasio : Building an Automated Bioinformatician: Choosing Input-Specific Parameter Choices for Biological Analysis
(15:40 – 16:00)	Guillaume Marçais : Generalization of the Minimizers Schemes
(16:00 – 16:20)	Fahad Alqahtani : Statistical Mitogenome Assembly with Repeats
(16:20 – 16:40)	Daniel Gibney : Algorithms for Genome Mappability

(16:40 – 17:00)	Business Meeting
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Saturday, October 27, 2018

Session I

(9:00 – 9:20)	Neda Tavakoli : Approximate Sequence Matching Algorithms to Handle Bounded Number of Errors
(9:20 – 9:40)	Kaden King : Expanding the Utility of Third Generation Sequencing with Mobile k-mer Counting
(9:40 – 10:00)	Anton Nekhai : Diagnosis of Facioscapulohumeral Dystrophy Through Nanopore Sequencing
(10:00 – 10:20)	Mark E. Royer : Java String-bioinformatics Libraries in Kawa Scheme

(10:20 – 10:40)	Break
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Session II

(10:40 – 11:00)	Pavel Avdeyev : Adequate Subgraph Approach for Guided Genome Halving Problem
(11:00 – 11:20)	Lorraine Ayad : CNEFinder: Finding Conserved Non-Coding Elements in Genomes
(11:20 – 11:40)	Ehdieh Khaledian : A Study of All Recognized Bacterial Phyla Using Network Science and Whole Proteome Clustering

(11:40 – 12:00)	Closing Remarks
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